



09/466 778

CORC

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Letters Patent of:
Hastings et al.

Docket No.: PF487

Patent No.: 6,872,546 **B1**

Issued: March 29, 2005

For: Hyaluronan-binding Protein and Encoding Genes

**REQUEST FOR CERTIFICATE OF CORRECTION
PURSUANT TO 37 CFR 1.322**

Attention: Certificate of Correction Branch
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Certificate
AUG 02 2005
of Correction

Sir:

Upon reviewing the above-identified patent, Patentee noted typographical errors which should be corrected.

At the Title Page:

Under the heading Other Publications, please correct the following reference as indicated:

--Lee et al., "A novel secretory Tumor Necrosis Factor-inducible Protein (TSG-6) is a ~~member~~ member of the family of Hyaluronate Binding Proteins, closely related to the Adhesion Receptor CD44" Jan. 1992, vol. 116, No. 2, pp. 545-557.* --.

In the Claims:

In Claim 33, page 317, lines 11-19, please delete the second subsets (a)-(g).

In Claim 46, page 318, line 9, after the phrase "claim 33," please insert --wherein said--.

Sequence Listing:

Patentees respectfully note that the entire Sequence Listing has been omitted from the issued patent. The Sequence Listing last filed by Patentees was a 37-page document filed on December 18, 2003. Accordingly, Patentees respectfully request that the last filed Sequence Listing be included in the Certificate of Correction issued by the Office, as suggested in the proposed Certificate of Correction submitted concurrently herewith. Should the Office wish to

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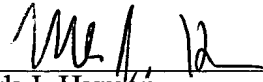
insert the Sequence Listing in some other manner, please contact the undersigned for any assistance deemed necessary.

The errors were not in the application as filed by applicant; accordingly no fee is required.

Transmitted herewith is a proposed Certificate of Correction effecting such amendments. Patentee respectfully solicits the granting of the requested Certificate of Correction.

Dated: 7/29/2005

Respectfully submitted,

By 
Mark J. Hyman

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PATENT NO. : 6,872,546 *B1*
APPLICATION NO. : 09/466,778
ISSUE DATE : March 29, 2005
INVENTOR(S) : Hastings et al.

It is certified that an error appears or errors appear in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

At the Title Page:

Under the heading Other Publications, please correct the fourth reference as follows:

--Lee et al., "A novel secretory Tumor Necrosis Factor-inducible Protein (TSG-6) is a ~~member~~ member of the family of Hyaluronate Binding Proteins, closely related to the Adhesion Receptor CD44" Jan. 1992, vol. 116, No. 2, pp. 545-557.* --.

In the Claims:

In Claim 33, at page 317, lines 11-19, please delete the second subsets (a)-(g).

In Claim 46, at page 318, line 9, after the phrase "claim 33," please insert --wherein said--.

Sequence Listing:

At page 315, immediately before the claims, please insert the following Sequence Listing:

SEQUENCE LISTING

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PATENT NO. 6,872,546 *B1*

Page 8 of 60

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Page 9 of 60

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ttc aca atg ctg tgg ccc aca gac gcc gcc ttt cga gct ctg cct ccg 4258
Phe Thr Met Leu Trp Pro Thr Asp Ala Ala Phe Arg Ala Leu Pro Pro
1350 1355 1360

gat cgc cag gcc tgg ctg tac cat gag gac cac cgt gac aag cta gca 4306
Asp Arg Gln Ala Trp Leu Tyr His Glu Asp His Arg Asp Lys Leu Ala
1365 1370 1375

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gcc att ctg cgg ggc cac atg att cgc aat gtc gag gcc ttg gca tct 4354
Ala Ile Leu Arg Gly His Met Ile Arg Asn Val Glu Ala Leu Ala Ser
1380 1385 1390 1395

gac ctg ccc aac ctg ggc cca ctt cga acc atg cat ggg acc ccc atc 4402
Asp Leu Pro Asn Leu Gly Pro Leu Arg Thr Met His Gly Thr Pro Ile
1400 1405 1410

tct ttc tcc tgc agc cga acg cgg ccc ggt gag ctc atg gtg ggt gag 4450
Ser Phe Ser Cys Ser Arg Thr Arg Pro Gly Glu Leu Met Val Gly Glu
1415 1420 1425

gat gat gct cgc att gtg cag cgg cac ttg ccc ttt gag ggt ggc ctg 4498
Asp Asp Ala Arg Ile Val Gln Arg His Leu Pro Phe Glu Gly Gly Leu
1430 1435 1440

gcc tat ggc atc gac cag ctg ctg gag cca cct ggc ctt ggt gct cgc 4546
Ala Tyr Gly Ile Asp Gln Leu Leu Glu Pro Pro Gly Leu Gly Ala Arg
1445 1450 1455

tgt gac cac ttt gag acc cgg ccc ctg cga ctg aac acc tgc agc atc 4594
Cys Asp His Phe Glu Thr Arg Pro Leu Arg Leu Asn Thr Cys Ser Ile
1460 1465 1470 1475

tgt ggg ctg gag cca ccc tgt cct gag ggg tca cag gag cag ggc agc 4642
Cys Gly Leu Glu Pro Pro Cys Pro Glu Gly Ser Gln Glu Gln Gly Ser
1480 1485 1490

cct gag gcc tgc tgg cgc ttc tac ccg aag ttc tgg acg tcc cct ccg 4690
Pro Glu Ala Cys Trp Arg Phe Tyr Pro Lys Phe Trp Thr Ser Pro Pro
1495 1500 1505

ctg cac tct ttg gga tta cgc agc gtc tgg gtc cac ccc agc ctt tgg 4738
Leu His Ser Leu Gly Leu Arg Ser Val Trp Val His Pro Ser Leu Trp
1510 1515 1520

ggt agg ccc caa ggc ctg ggc agg ggc tgc cac cgc aat tgt gtc acc 4786
Gly Arg Pro Gln Gly Leu Gly Arg Gly Cys His Arg Asn Cys Val Thr
1525 1530 1535

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<p>acc acc tgg aag ccc agc tgc tgc cct ggt cac tat ggc agt gag tgc Thr Thr Trp Lys Pro Ser Cys Cys Pro Gly His Tyr Gly Ser Glu Cys 1540 1545 1550 1555</p>	4834
<p>caa gct tgc cct ggc ggc ccc agc agc cct tgt agt gac cgt ggc gtg Gln Ala Cys Pro Gly Gly Pro Ser Ser Pro Cys Ser Asp Arg Gly Val 1560 1565 1570</p>	4882
<p>tgc atg gac ggc atg agt ggc agt ggg cag tgt ctg tgc cgt tca ggt Cys Met Asp Gly Met Ser Gly Ser Gly Gln Cys Leu Cys Arg Ser Gly 1575 1580 1585</p>	4930
<p>ttt gct ggg aca gcc tgt gaa ctc tgt gct cct ggt gcc ttt ggg ccc Phe Ala Gly Thr Ala Cys Glu Leu Cys Ala Pro Gly Ala Phe Gly Pro 1590 1595 1600</p>	4978
<p>cat tgt caa gcc tgc cgc tgc act gtg cat ggc cgc tgt gat gag ggc His Cys Gln Ala Cys Arg Cys Thr Val His Gly Arg Cys Asp Glu Gly 1605 1610 1615</p>	5026
<p>ctt ggg ggc tct ggc tcc tgc ttc tgt gat gaa ggc tgg act ggg cca Leu Gly Gly Ser Gly Ser Cys Phe Cys Asp Glu Gly Trp Thr Gly Pro 1620 1625 1630 1635</p>	5074
<p>cgc tgt gag gtg caa ctg gag ctg cag cct gtg tgt acc cca ccc tgt Arg Cys Glu Val Gln Leu Glu Leu Gln Pro Val Cys Thr Pro Pro Cys 1640 1645 1650</p>	5122
<p>gca ccc gag gct gtg tgc cgt gca ggc aac agc tgt gag tgc agc ctg Ala Pro Glu Ala Val Cys Arg Ala Gly Asn Ser Cys Glu Cys Ser Leu 1655 1660 1665</p>	5170
<p>ggc tat gaa ggg gat ggc cgt gtg tgt aca gtg gca gac ctg tgc cag Gly Tyr Glu Gly Asp Gly Arg Val Cys Thr Val Ala Asp Leu Cys Gln 1670 1675 1680</p>	5218
<p>gac ggg cat ggt ggc tgc agt gag cac gcc aac tgt agc cag gta gga Asp Gly His Gly Gly Cys Ser Glu His Ala Asn Cys Ser Gln Val Gly 1685 1690 1695</p>	5266

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aca atg gtc act tgt acc tgc ctg ccc gac tac gag ggt gat ggc tgg 5314
Thr Met Val Thr Cys Thr Cys Leu Pro Asp Tyr Glu Gly Asp Gly Trp
1700 1705 1710 1715

agc tgc cgg gcc cgc aac ccc tgc aca gat ggc cac cgc ggg ggc tgc 5362
 Ser Cys Arg Ala Arg Asn Pro Cys Thr Asp Gly His Arg Gly Gly Cys
 1720 1725 1730

agc gag cac gcc aac tgc ttg agc acc ggc ctg aac aca cgg cgc tgt 5410
 Ser Glu His Ala Asn Cys Leu Ser Thr Gly Leu Asn Thr Arg Arg Cys
 1735 1740 1745

gag tgc cac gca ggc tac gta ggc gat gga ctg cag tgt ctg gag gag 5458
Glu Cys His Ala Gly Tyr Val Gly Asp Gly Leu Gln Cys Leu Glu Glu
1750 1755 1760

tcg gaa cca cct gtg gac cgc tgc ttg ggc cag cca ccg ccc tgc cac 5506
Ser Glu Pro Pro Val Asp Arg Cys Leu Gly Gln Pro Pro Pro Cys His
1765 1770 1775

tca gat gcc atg tgc act gac ctg cac ttc cag gag aaa cgg gct ggc 5554
Ser Asp Ala Met Cys Thr Asp Leu His Phe Gln Glu Lys Arg Ala Gly
1780 1785 1790 1795

ggt ttc cac ctc cag gcc acc agc ggc cct tat ggt ctg aac ttt tcg 5602
Val Phe His Leu Gln Ala Thr Ser Gly Pro Tyr Gly Leu Asn Phe Ser
1800 1805 1810

gag gct gag gcg gca tgc gaa gca cag gga gcc gtc ctt gct tca ttc 5650
Glu Ala Glu Ala Ala Cys Glu Ala Gln Gly Ala Val Leu Ala Ser Phe
1815 1820 1825

cct cag ctc tct gct gcc cag cag ctg ggc ttc cac ctg tgc ctc atg 5698
Pro Gln Leu Ser Ala Ala Gln Gln Leu Gly Phe His Leu Cys Leu Met
1830 1835 1840

ggc tgg ctg gcc aat ggc tcc act gcc cac cct gtg gtt ttc cct gtg 5746
Gly Trp Leu Ala Asn Gly Ser Thr Ala His Pro Val Val Phe Pro Val
1845 1850 1855

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gcg gac tgt ggc aat ggt cgg gtg ggc ata gtc agc ctg ggt gcc cgc Ala Asp Cys Gly Asn Gly Arg Val Gly Ile Val Ser Leu Gly Ala Arg 1860	1865	1870	1875	5794
aag aac ctc tca gaa cgc tgg gat gcc tac tgc ttc cgt gtg caa gat Lys Asn Leu Ser Glu Arg Trp Asp Ala Tyr Cys Phe Arg Val Gln Asp 1880	1885	1890		5842
gtg gcc tgc cga tgc cga aat ggc ttc gtg ggt gac ggg atc agc acg Val Ala Cys Arg Cys Arg Asn Gly Phe Val Gly Asp Gly Ile Ser Thr 1895	1900	1905		5890
tgc aat ggg aag ctg ctg gat gtg ctg gct gcc act gcc aac ttc tcc Cys Asn Gly Lys Leu Leu Asp Val Leu Ala Ala Thr Ala Asn Phe Ser 1910	1915	1920		5938
acc ttc tat ggg atg cta ttg ggc tat gcc aat gcc acc cag cgg ggt Thr Phe Tyr Gly Met Leu Leu Gly Tyr Ala Asn Ala Thr Gln Arg Gly 1925	1930	1935		5986
ctc gac ttc ctg gac ttc ctg gat gat gag ctc acg tat aag aca ctc Leu Asp Phe Leu Asp Phe Leu Asp Asp Glu Leu Thr Tyr Lys Thr Leu 1940	1945	1950	1955	6034
ttc gtc cct gtc aat gaa ggc ttt gtg gac aac atg acg ctg agt ggc Phe Val Pro Val Asn Glu Gly Phe Val Asp Asn Met Thr Leu Ser Gly 1960	1965	1970		6082
cca aac ttg gag ctg cat gcc tcc aac gcc acc ctc cta agt gcc aac Pro Asn Leu Glu Leu His Ala Ser Asn Ala Thr Leu Leu Ser Ala Asn 1975	1980	1985		6130
gcc agc cag ggg aag ttg ctt ccg gcc cac tca ggc ctc agc ctc atc Ala Ser Gln Gly Lys Leu Leu Pro Ala His Ser Gly Leu Ser Leu Ile 1990	1995	2000		6178
atc agt gac gca ggc cct gac aac agt tcc tgg gcc cct gtg gcc cca Ile Ser Asp Ala Gly Pro Asp Asn Ser Ser Trp Ala Pro Val Ala Pro 2005	2010	2015		6226

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nctgagggcc tgtcccagac aatannngtn ccctcgag 6761

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 <212> PRT
 <213> Homo sapiens

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 <223> Xaa equals any of the naturally occurring L-amino acids

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 20 25 30
 Ala Ser Leu Ala Gln Gln Leu Cys Arg Gln His Ile Ile Ala Gly Gln
 35 40 45
 His Ile Leu Glu Asp Thr Arg Thr Gln Gln Thr Arg Arg Trp Trp Thr
 50 55 60

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Leu	Ala	Gly	Gln	Glu	Ile	Thr	Val	Thr	Phe	Asn	Gln	Phe	Thr	Lys	Tyr	
65					70					75					80	
Ser	Tyr	Lys	Tyr	Lys	Asp	Gln	Pro	Gln	Gln	Thr	Phe	Asn	Ile	Tyr	Lys	
				85					90					95		
Ala	Asn	Asn	Ile	Ala	Ala	Asn	Gly	Val	Phe	His	Val	Val	Thr	Gly	Leu	
			100					105					110			
Arg	Trp	Gln	Ala	Pro	Ser	Gly	Thr	Pro	Gly	Asp	Pro	Lys	Arg	Thr	Ile	
		115					120					125				
Gly	Gln	Ile	Leu	Ala	Ser	Thr	Glu	Ala	Phe	Ser	Arg	Phe	Glu	Thr	Ile	
	130					135					140					
Leu	Glu	Asn	Cys	Gly	Leu	Pro	Ser	Ile	Leu	Asp	Gly	Pro	Gly	Pro	Phe	
145					150					155					160	
Thr	Val	Phe	Ala	Pro	Ser	Asn	Glu	Ala	Val	Asp	Ser	Leu	Arg	Asp	Gly	
				165					170					175		
Arg	Leu	Ile	Tyr	Leu	Phe	Thr	Ala	Gly	Leu	Ser	Lys	Leu	Gln	Glu	Leu	
			180					185					190			
Val	Arg	Tyr	His	Ile	Tyr	Asn	His	Gly	Gln	Leu	Thr	Val	Glu	Lys	Leu	
		195					200					205				
Ile	Ser	Lys	Gly	Arg	Ile	Leu	Thr	Met	Ala	Asn	Gln	Val	Leu	Ala	Val	
	210					215					220					
Asn	Ile	Ser	Glu	Glu	Gly	Arg	Ile	Leu	Leu	Gly	Pro	Glu	Gly	Val	Pro	
225					230					235					240	
Leu	Gln	Arg	Val	Asp	Val	Met	Ala	Ala	Asn	Gly	Val	Ile	His	Met	Leu	
				245					250					255		
Asp	Gly	Ile	Leu	Leu	Pro	Pro	Thr	Ile	Leu	Pro	Ile	Leu	Pro	Lys	His	
			260					265					270			
Cys	Ser	Glu	Glu	Gln	His	Lys	Ile	Val	Ala	Gly	Ser	Cys	Val	Asp	Cys	
		275					280					285				

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Gln	Ala	Leu	Asn	Thr	Ser	Thr	Cys	Pro	Pro	Asn	Ser	Val	Lys	Leu	Asp
	290						295					300			
Ile	Phe	Pro	Lys	Glu	Cys	Val	Tyr	Ile	His	Asp	Pro	Thr	Gly	Leu	Asn
305					310					315					320
Val	Leu	Lys	Lys	Gly	Cys	Ala	Ser	Tyr	Cys	Asn	Gln	Thr	Ile	Met	Glu
				325					330					335	
Gln	Gly	Cys	Cys	Lys	Gly	Phe	Phe	Gly	Pro	Asp	Cys	Thr	Gln	Cys	Pro
			340					345					350		
Gly	Gly	Phe	Ser	Asn	Pro	Cys	Tyr	Gly	Lys	Gly	Asn	Cys	Ser	Asp	Gly
	355						360					365			
Ile	Gln	Gly	Asn	Gly	Ala	Cys	Leu	Cys	Phe	Pro	Asp	Tyr	Lys	Gly	Ile
370						375					380				
Ala	Cys	His	Ile	Cys	Ser	Asn	Pro	Asn	Lys	His	Gly	Glu	Gln	Cys	Gln
385					390					395					400
Glu	Asp	Cys	Gly	Cys	Val	His	Gly	Leu	Cys	Asp	Asn	Arg	Pro	Gly	Ser
				405					410					415	
Gly	Gly	Val	Cys	Gln	Gln	Gly	Thr	Cys	Ala	Pro	Gly	Phe	Ser	Gly	Arg
			420					425					430		
Phe	Cys	Asn	Glu	Ser	Met	Gly	Asp	Cys	Gly	Pro	Thr	Gly	Leu	Ala	Gln
	435						440					445			
His	Cys	His	Leu	His	Ala	Arg	Cys	Val	Ser	Gln	Glu	Gly	Val	Ala	Arg
450						455					460				
Cys	Arg	Cys	Leu	Asp	Gly	Phe	Glu	Gly	Asp	Gly	Phe	Ser	Cys	Thr	Pro
465					470					475					480
Ser	Asn	Pro	Cys	Ser	His	Pro	Asp	Arg	Gly	Gly	Cys	Ser	Glu	Asn	Ala
				485					490					495	
Glu	Cys	Val	Pro	Gly	Ser	Leu	Gly	Thr	His	His	Cys	Thr	Cys	His	Lys
			500					505					510		

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Gly Trp Ser Gly Asp Gly Arg Val Cys Val Ala Ile Asp Glu Cys Glu	515	520	525
Leu Asp Val Arg Gly Gly Cys His Thr Asp Ala Leu Cys Ser Tyr Val	530	535	540
Gly Pro Gly Gln Ser Arg Cys Thr Cys Lys Leu Gly Phe Ala Gly Asp	545	550	555
Gly Tyr Gln Cys Ser Pro Ile Asp Pro Cys Arg Ala Gly Asn Gly Gly	565	570	575
Cys His Gly Leu Glu Leu Glu Ala Asn Ala His Phe Ser Ile Phe Tyr	580	585	590
Gln Trp Leu Lys Ser Ala Gly Ile Thr Leu Pro Ala Asp Arg Arg Val	595	600	605
Thr Ala Leu Val Pro Ser Glu Ala Ala Val Arg Gln Leu Ser Pro Glu	610	615	620
Asp Arg Ala Phe Trp Leu Gln Pro Arg Thr Leu Pro Asn Leu Val Arg	625	630	635
Ala His Phe Leu Gln Gly Ala Leu Phe Glu Glu Glu Leu Ala Arg Leu	645	650	655
Gly Gly Gln Glu Val Ala Thr Leu Asn Pro Thr Thr Arg Trp Glu Ile	660	665	670
Arg Asn Ile Ser Gly Arg Val Trp Val Gln Asn Ala Ser Val Asp Val	675	680	685
Ala Asp Leu Leu Ala Thr Asn Gly Val Leu His Ile Leu Ser Gln Val	690	695	700
Leu Leu Pro Pro Arg Gly Asp Val Pro Gly Gly Gln Gly Leu Leu Gln	705	710	715
Gln Leu Asp Leu Val Pro Ala Phe Ser Leu Phe Arg Glu Leu Leu Gln	725	730	735

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His	His	Gly	Leu	Val	Pro	Gln	Ile	Glu	Ala	Ala	Thr	Ala	Tyr	Thr	Ile	
			740					745					750			
Phe	Val	Pro	Thr	Asn	Arg	Ser	Leu	Glu	Ala	Gln	Gly	Asn	Ser	Ser	His	
		755					760					765				
Leu	Asp	Ala	Asp	Thr	Val	Arg	His	His	Val	Val	Leu	Gly	Glu	Ala	Leu	
	770					775					780					
Ser	Met	Glu	Thr	Leu	Arg	Lys	Gly	Gly	His	Arg	Asn	Ser	Leu	Leu	Gly	
785					790					795					800	
Pro	Ala	His	Trp	Ile	Val	Phe	Tyr	Asn	His	Ser	Gly	Gln	Pro	Glu	Val	
				805					810					815		
Asn	His	Val	Pro	Leu	Glu	Gly	Pro	Met	Leu	Glu	Ala	Pro	Gly	Arg	Ser	
			820					825					830			
Leu	Ile	Gly	Leu	Ser	Gly	Val	Leu	Thr	Val	Gly	Ser	Ser	Arg	Cys	Leu	
	835						840					845				
His	Ser	His	Ala	Glu	Ala	Leu	Arg	Glu	Lys	Cys	Val	Asn	Cys	Thr	Arg	
	850					855					860					
Arg	Phe	Arg	Cys	Thr	Gln	Gly	Phe	Gln	Leu	Gln	Asp	Thr	Pro	Arg	Lys	
865					870					875					880	
Ser	Cys	Val	Tyr	Arg	Ser	Gly	Phe	Ser	Phe	Ser	Arg	Gly	Cys	Ser	Tyr	
				885					890					895		
Thr	Cys	Ala	Lys	Lys	Ile	Gln	Val	Pro	Asp	Cys	Cys	Pro	Gly	Phe	Phe	
		900						905					910			
Gly	Thr	Leu	Cys	Glu	Pro	Cys	Pro	Gly	Gly	Leu	Gly	Gly	Val	Cys	Ser	
		915					920					925				
Gly	His	Gly	Gln	Cys	Gln	Asp	Arg	Phe	Leu	Gly	Ser	Gly	Glu	Cys	His	
	930					935					940					
Cys	His	Glu	Gly	Phe	His	Gly	Thr	Ala	Cys	Glu	Val	Cys	Glu	Leu	Gly	
945					950					955					960	

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Arg Tyr Gly Pro	Asn Cys Thr Gly Val	Cys Asp Cys Ala His Gly Leu	
	965	970	975
Cys Gln Glu Gly	Leu Gln Gly Asp	Gly Ser Cys Val	Cys Asn Val Gly
980	985	990	
Trp Gln Gly Leu	Arg Cys Asp Gln	Lys Ile Thr Ser	Pro Gln Cys Pro
995	1000	1005	
Arg Lys Cys Asp	Pro Asn Ala Asn Cys Val	Gln Asp Ser Ala Gly Ala	
1010	1015	1020	
Ser Thr Cys Ala	Cys Ala Ala Gly Tyr	Ser Gly Asn Gly Ile Phe Cys	
1025	1030	1035	1040
Ser Glu Val Asp	Pro Cys Ala His Gly His	Gly Gly Cys Ser Pro His	
1045	1050	1055	
Ala Asn Cys Thr	Lys Val Ala Pro Gly	Gln Arg Thr Cys Thr Cys Gln	
1060	1065	1070	
Asp Gly Tyr Met	Gly Asp Gly Glu Leu Cys Gln Glu Ile	Asn Ser Cys	
1075	1080	1085	
Leu Ile His His	Gly Gly Cys His Ile His Ala Glu	Cys Ile Pro Thr	
1090	1095	1100	
Gly Pro Gln Gln	Val Ser Cys Ser Cys Arg Glu	Gly Tyr Ser Gly Asp	
1105	1110	1115	1120
Gly Ile Arg Thr	Cys Glu Leu Leu Asp Pro	Cys Ser Lys Asn Asn Gly	
1125	1130	1135	
Gly Cys Ser Pro	Tyr Ala Thr Cys Lys Ser Thr Gly Asp	Gly Gln Arg	
1140	1145	1150	
Thr Cys Thr Cys	Asp Thr Ala His Thr Val Gly Asp	Gly Leu Thr Cys	
1155	1160	1165	
Arg Ala Arg Val	Gly Leu Glu Leu Leu Arg Asp Lys	His Ala Ser Phe	
1170	1175	1180	

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Phe	Ser	Leu	Arg	Leu	Leu	Glu	Tyr	Lys	Glu	Leu	Lys	Gly	Asp	Gly	Pro
1185					1190					1195					1200
Phe	Thr	Ile	Phe	Val	Pro	His	Ala	Asp	Leu	Met	Ser	Asn	Leu	Ser	Gln
				1205					1210					1215	
Asp	Glu	Leu	Ala	Arg	Ile	Arg	Ala	His	Arg	Gln	Leu	Val	Phe	Arg	Tyr
			1220					1225						1230	
His	Val	Val	Gly	Cys	Arg	Arg	Leu	Arg	Ser	Glu	Asp	Leu	Leu	Glu	Gln
			1235				1240						1245		
Gly	Tyr	Ala	Thr	Ala	Leu	Ser	Gly	His	Pro	Leu	Arg	Phe	Ser	Glu	Arg
	1250					1255					1260				
Glu	Gly	Ser	Ile	Tyr	Leu	Asn	Asp	Phe	Ala	Arg	Val	Val	Ser	Ser	Asp
1265					1270					1275					1280
His	Glu	Ala	Val	Asn	Gly	Ile	Leu	His	Phe	Ile	Asp	Arg	Val	Leu	Leu
				1285					1290					1295	
Pro	Pro	Glu	Ala	Leu	His	Trp	Glu	Pro	Asp	Asp	Ala	Pro	Ile	Pro	Arg
			1300					1305					1310		
Arg	Asn	Val	Thr	Ala	Ala	Ala	Gln	Gly	Phe	Gly	Tyr	Lys	Ile	Phe	Ser
		1315					1320						1325		
Gly	Leu	Leu	Lys	Val	Ala	Gly	Leu	Leu	Pro	Leu	Leu	Arg	Glu	Ala	Ser
	1330					1335					1340				
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1345					1350					1355					1360
Leu	Pro	Pro	Asp	Arg	Gln	Ala	Trp	Leu	Tyr	His	Glu	Asp	His	Arg	Asp
				1365					1370					1375	
Lys	Leu	Ala	Ala	Ile	Leu	Arg	Gly	His	Met	Ile	Arg	Asn	Val	Glu	Ala
			1380					1385						1390	
Leu	Ala	Ser	Asp	Leu	Pro	Asn	Leu	Gly	Pro	Leu	Arg	Thr	Met	His	Gly
		1395					1400					1405			

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Thr	Pro	Ile	Ser	Phe	Ser	Cys	Ser	Arg	Thr	Arg	Pro	Gly	Glu	Leu	Met
	1410					1415					1420				
Val	Gly	Glu	Asp	Asp	Ala	Arg	Ile	Val	Gln	Arg	His	Leu	Pro	Phe	Glu
1425					1430					1435					1440
Gly	Gly	Leu	Ala	Tyr	Gly	Ile	Asp	Gln	Leu	Leu	Glu	Pro	Pro	Gly	Leu
				1445					1450					1455	
Gly	Ala	Arg	Cys	Asp	His	Phe	Glu	Thr	Arg	Pro	Leu	Arg	Leu	Asn	Thr
			1460					1465					1470		
Cys	Ser	Ile	Cys	Gly	Leu	Glu	Pro	Pro	Cys	Pro	Glu	Gly	Ser	Gln	Glu
		1475					1480					1485			
Gln	Gly	Ser	Pro	Glu	Ala	Cys	Trp	Arg	Phe	Tyr	Pro	Lys	Phe	Trp	Thr
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Ser	Pro	Pro	Leu	His	Ser	Leu	Gly	Leu	Arg	Ser	Val	Trp	Val	His	Pro
1505					1510					1515					1520
Ser	Leu	Trp	Gly	Arg	Pro	Gln	Gly	Leu	Gly	Arg	Gly	Cys	His	Arg	Asn
				1525					1530					1535	
Cys	Val	Thr	Thr	Thr	Trp	Lys	Pro	Ser	Cys	Cys	Pro	Gly	His	Tyr	Gly
				1540				1545					1550		
Ser	Glu	Cys	Gln	Ala	Cys	Pro	Gly	Gly	Pro	Ser	Ser	Pro	Cys	Ser	Asp
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Phe	Gly	Pro	His	Cys	Gln	Ala	Cys	Arg	Cys	Thr	Val	His	Gly	Arg	Cys
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Asp	Glu	Gly	Leu	Gly	Gly	Ser	Gly	Ser	Cys	Phe	Cys	Asp	Glu	Gly	Trp
			1620					1625					1630		

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Thr Gly Pro	Arg Cys Glu Val Gln	Leu Glu Leu Gln Pro	Val Cys Thr
1635	1640	1645	
Pro Pro Cys Ala Pro Glu Ala	Val Cys Arg Ala Gly	Asn Ser Cys Glu	
1650	1655	1660	
Cys Ser Leu Gly Tyr Glu	Gly Asp Gly Arg Val	Cys Thr Val Ala Asp	
1665	1670	1675	1680
Leu Cys Gln Asp Gly	His Gly Gly Cys Ser	Glu His Ala Asn Cys Ser	
1685	1690	1695	
Gln Val Gly Thr	Met Val Thr Cys Thr	Cys Leu Pro Asp Tyr	Glu Gly
1700	1705	1710	
Asp Gly Trp	Ser Cys Arg Ala Arg	Asn Pro Cys Thr Asp	Gly His Arg
1715	1720	1725	
Gly Gly Cys Ser Glu His Ala	Asn Cys Leu Ser Thr	Gly Leu Asn Thr	
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Arg Arg Cys Glu Cys His	Ala Gly Tyr Val Gly	Asp Gly Leu Gln Cys	
1745	1750	1755	1760
Leu Glu Glu Ser Glu	Pro Pro Val Asp Arg	Cys Leu Gly Gln Pro	Pro
1765	1770	1775	
Pro Cys His Ser	Asp Ala Met Cys Thr	Asp Leu His Phe Gln	Glu Lys
1780	1785	1790	
Arg Ala Gly	Val Phe His Leu Gln	Ala Thr Ser Gly Pro	Tyr Gly Leu
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Asn Phe Ser Glu Ala Glu Ala	Ala Cys Glu Ala Gln	Gly Ala Val Leu	
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Ala Ser Phe Pro Gln Leu	Ser Ala Ala Gln Gln	Leu Gly Phe His Leu	
1825	1830	1835	1840
Cys Leu Met Gly Trp	Leu Ala Asn Gly Ser	Thr Ala His Pro Val	Val
1845	1850	1855	

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Phe Pro Val Ala	Asp Cys Gly Asn Gly	Arg Val Gly Ile Val	Ser Leu
1860	1865	1870	
Gly Ala Arg Lys Asn Leu Ser Glu Arg Trp Asp Ala Tyr Cys Phe Arg			
1875	1880	1885	
Val Gln Asp Val Ala Cys Arg Cys Arg Asn Gly Phe Val Gly Asp Gly			
1890	1895	1900	
Ile Ser Thr Cys Asn Gly Lys Leu Leu Asp Val Leu Ala Ala Thr Ala			
1905	1910	1915	1920
Asn Phe Ser Thr Phe Tyr Gly Met Leu Leu Gly Tyr Ala Asn Ala Thr			
1925	1930	1935	
Gln Arg Gly Leu Asp Phe Leu Asp Phe Leu Asp Asp Glu Leu Thr Tyr			
1940	1945	1950	
Lys Thr Leu Phe Val Pro Val Asn Glu Gly Phe Val Asp Asn Met Thr			
1955	1960	1965	
Leu Ser Gly Pro Asn Leu Glu Leu His Ala Ser Asn Ala Thr Leu Leu			
1970	1975	1980	
Ser Ala Asn Ala Ser Gln Gly Lys Leu Leu Pro Ala His Ser Gly Leu			
1985	1990	1995	2000
Ser Leu Ile Ile Ser Asp Ala Gly Pro Asp Asn Ser Ser Trp Ala Pro			
2005	2010	2015	
Val Ala Pro Gly Thr Val Val Val Ser Arg Ile Ile Val Trp Asp Ile			
2020	2025	2030	
Met Ala Phe Asn Gly Ile Ile His Ala Leu Ala Ser Pro Leu Leu Ala			
2035	2040	2045	
Pro Pro Gln Pro Gln Ala Val Leu Ala Xaa Glu Ala Pro Pro Val Ala			
2050	2055	2060	
Ala Gly Val Gly Ala Val Leu Ala Ala Gly Ala Leu Leu Gly Leu Val			
2065	2070	2075	2080

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Ala Gly Ala Leu Tyr Leu Arg Ala Arg Gly Lys Pro Met Gly Phe Gly
2085 2090 2095

Phe Ser Ala Phe Gln Ala Glu Asp Asp Ala Asp Asp Xaa Phe Ser Pro
2100 2105 2110

Trp Gln Glu Gly Thr Asn Pro Xaa Leu Xaa Xaa Val Pro Asn Pro Val
2115 2120 2125

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Lys Gly His Val Cys Ala Ala Gly Trp Met Ala Lys Gly Arg Val Gly
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Tyr Val Lys Gly Asn Cys Gly Gly Lys Thr Gly Asp Tyr Gly Arg Asn
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Arg Ser Arg Trp Asp Ala Tyr Cys Tyr Asn His Ala Lys Cys Gly Gly
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Val	Thr	Asp	Lys	Arg	Lys	Ser	Gly	Asn	Tyr	Asp	Asn	Cys	Tyr	Trp	His
			100					105					110		

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Arg Lys Tyr Gly Arg His Ser Asp Asp Asp Asp Gly Cys Ala Asp Tyr	115	120	125
Val Tyr Asp Ser Tyr Asp Asp Val His Gly Val Gly Arg Tyr Cys Gly	130	135	140
Asp Asp Asp Ser Thr Gly Asn Val Met Thr Lys Ser Asp Ala Ser Val	145	150	155
Thr Ala Gly Gly Lys Tyr Val Ala Met Asp Val Ser Lys Ser Ser Gly	165	170	175
Lys Asn Thr Ser Thr Thr Ser Thr Gly Asn Lys Asn Ala Gly Arg Ser	180	185	190

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<p>gac tac gag ggt gat ggc tgg agc tgc cgg gcc cgc aac ccc tgc aca Asp Tyr Glu Gly Asp Gly Trp Ser Cys Arg Ala Arg Asn Pro Cys Thr 10 15 20</p>	102
<p>gat ggc cac cgc ggg ggc tgc agc gag cac gcc aac tgc ttg agc acc Asp Gly His Arg Gly Gly Cys Ser Glu His Ala Asn Cys Leu Ser Thr 25 30 35 40</p>	150
<p>ggc ctg aac aca cgg cgc tgt gag tgc cac gca ggc tac gta ggc gat Gly Leu Asn Thr Arg Arg Cys Glu Cys His Ala Gly Tyr Val Gly Asp 45 50 55</p>	198
<p>gga ctg cag tgt ctg gag gag tcg gaa cca cct gtg gac cgc tgc ttg Gly Leu Gln Cys Leu Glu Glu Ser Glu Pro Pro Val Asp Arg Cys Leu 60 65 70</p>	246
<p>ggc cag cca ccg ccc tgc cac tca gat gcc atg tgc act gac ctg cac Gly Gln Pro Pro Pro Cys His Ser Asp Ala Met Cys Thr Asp Leu His 75 80 85</p>	294
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<p>cct tat ggt ctg aac ttt tcg gag gct gag gcg gca tgc gaa gca cag Pro Tyr Gly Leu Asn Phe Ser Glu Ala Glu Ala Ala Cys Glu Ala Gln 105 110 115 120</p>	390
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<p>ata gtc agc ctg ggt gcc cgc aag aac ctc tca gaa cgc tgg gat gcc Ile Val Ser Leu Gly Ala Arg Lys Asn Leu Ser Glu Arg Trp Asp Ala 170 175 180</p>	582
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<p>gtg ggt gac ggg atc agc acg tgc aat ggg aag ctg ctg gat gtg ctg Val Gly Asp Gly Ile Ser Thr Cys Asn Gly Lys Leu Leu Asp Val Leu 205 210 215</p>	678
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<p>gcc aat gcc acc cag cgg ggt ctc gac ttc ctg gac ttc ctg gat gat Ala Asn Ala Thr Gln Arg Gly Leu Asp Phe Leu Asp Phe Leu Asp Asp 235 240 245</p>	774
<p>gag ctc acg tat aag aca ctc ttc gtc cct gtc aat gaa ggc ttt gtg Glu Leu Thr Tyr Lys Thr Leu Phe Val Pro Val Asn Glu Gly Phe Val 250 255 260</p>	822
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<p>gcc acc ctc cta agt gcc aac gcc agc cag ggg aag ttg ctt ccg gcc Ala Thr Leu Leu Ser Ala Asn Ala Ser Gln Gly Lys Leu Leu Pro Ala 285 290 295</p>	918
<p>cac tca ggc ctc agc ctc atc atc agt gac gca ggc cct gac aac agt His Ser Gly Leu Ser Leu Ile Ile Ser Asp Ala Gly Pro Asp Asn Ser 300 305 310</p>	966
<p>tcc tgg gcc cct gtg gcc cca ggg aca gtt gtg gtt agc cgt atc att Ser Trp Ala Pro Val Ala Pro Gly Thr Val Val Val Ser Arg Ile Ile 315 320 325</p>	1014

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ccc ctc ctg gca ccc cca cag ccc cag gca gtg ctg gcg cnt gaa gcc Pro Leu Leu Ala Pro Pro Gln Pro Gln Ala Val Leu Ala Xaa Glu Ala 345 350 355 360	1110
cca cct gtg gcg gca ggc gtg ggg gct gtg ctt gcc gct gga gca ctg Pro Pro Val Ala Ala Gly Val Gly Ala Val Leu Ala Ala Gly Ala Leu 365 370 375	1158
ctt ggc ttg gtg gcc gga gct ctc tac ctc cgt gcc cga ggc aag ccc Leu Gly Leu Val Ala Gly Ala Leu Tyr Leu Arg Ala Arg Gly Lys Pro 380 385 390	1206
atg ggc ttt ggc ttc tct gcc ttc cag gcg gaa gat gat gct gat gac Met Gly Phe Gly Phe Ser Ala Phe Gln Ala Glu Asp Asp Ala Asp Asp 395 400 405	1254
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Cys His Ala Gly Tyr Val Gly Asp Gly Leu Gln Cys Leu Glu Glu Ser
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Glu	Pro	Pro	Val	Asp	Arg	Cys	Leu	Gly	Gln	Pro	Pro	Pro	Cys	His	Ser
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Ala	Glu	Ala	Ala	Cys	Glu	Ala	Gln	Gly	Ala	Val	Leu	Ala	Ser	Phe	Pro
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Trp	Leu	Ala	Asn	Gly	Ser	Thr	Ala	His	Pro	Val	Val	Phe	Pro	Val	Ala
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Asp	Cys	Gly	Asn	Gly	Arg	Val	Gly	Ile	Val	Ser	Leu	Gly	Ala	Arg	Lys
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Asn	Leu	Ser	Glu	Arg	Trp	Asp	Ala	Tyr	Cys	Phe	Arg	Val	Gln	Asp	Val
			180					185					190		
Ala	Cys	Arg	Cys	Arg	Asn	Gly	Phe	Val	Gly	Asp	Gly	Ile	Ser	Thr	Cys
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Ser Gln Gly Lys Leu Leu Pro Ala His Ser Gly Leu Ser Leu Ile Ile
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Ser Asp Ala Gly Pro Asp Asn Ser Ser Trp Ala Pro Val Ala Pro Gly
305 310 315 320

Thr Val Val Val Ser Arg Ile Ile Val Trp Asp Ile Met Ala Phe Asn
325 330 335

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340 345 350

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Ala Ala Lys Ala Val Cys Gly Gly His Ala Thr Tyr Lys Ala Ala Arg
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atg ggc ctg ttg ctc ctg gtc cca ttg ctc ctg ctg ccc ggc tcc tac      165
Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu Leu Pro Gly Ser Tyr
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gga ctg ccc ttc tac tac ggc ttc tac tac tcc aac agc gcc aac gac      213
Gly Leu Pro Phe Tyr Tyr Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp
             20             25             30

cag aac cta ggc aac ggt cat ggc aaa gac cta cnt aat gga gtg aag      261
Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Xaa Asn Gly Val Lys
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ctg gtg gtg gag aca ccc gag gag acc ctg ttc acc tac caa ggg gcc      309
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agt gtg atc ctg ccc tgc cgc tac cgc tac gag ccg gcc ctg gtc tcc      357
Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser
             65             70             75             80

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cgc tgt gag gtc atn gac ggg ctg gag gat gaa agc ggt ctg gtg gag Arg Cys Glu Val Xaa Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu <div style="text-align: center;">145 150 155 160</div>	597
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gcg gtg gtg gcc tcc ttt gag cag ctc ttc cgg gcc tgg gag gag ggc Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly <div style="text-align: center;">195 200 205</div>	741
ctg gac tgg tgc aac gcg ggc tgg ctg cag gat gcc acg gtg cag tac Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr <div style="text-align: center;">210 215 220</div>	789
ccc atc atg ttg ccc cgg cag ccc tgc ggt ggc ccg gac ctg gca cct Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Asp Leu Ala Pro <div style="text-align: center;">225 230 235 240</div>	837

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cac	cct	gag	aan	ctg	acn	ctg	aca	naa	gca	agg	gaa	gcc	tgc	caa	gaa	981
His	Pro	Glu	Xaa	Leu	Xaa	Leu	Thr	Xaa	Ala	Arg	Glu	Ala	Cys	Gln	Glu	
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Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Xaa Asn Gly Val Lys
      35             40             45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala
      50             55             60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser
      65             70             75             80

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Pro	Arg	Arg	Val	Arg	Val	Lys	Trp	Trp	Lys	Leu	Ser	Glu	Asn	Gly	Ala	
				85					90					95		
Pro	Glu	Lys	Asp	Val	Leu	Val	Ala	Ile	Gly	Leu	Arg	His	Arg	Ser	Phe	
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Gly	Asp	Tyr	Gln	Gly	Arg	Val	His	Leu	Arg	Gln	Asp	Lys	Glu	His	Asp	
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Tyr	Gln	Phe	Asn	Phe	His	Glu	Gly	Gln	Gln	Val	Cys	Ala	Glu	Gln	Ala	
			180					185					190			
Ala	Val	Val	Ala	Ser	Phe	Glu	Gln	Leu	Phe	Arg	Ala	Trp	Glu	Glu	Gly	
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Pro	Ile	Met	Leu	Pro	Arg	Gln	Pro	Cys	Gly	Gly	Pro	Asp	Leu	Ala	Pro	
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Gly	Val	Arg	Ser	Tyr	Gly	Pro	Arg	His	Arg	Arg	Leu	His	Arg	Tyr	Asp	
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Val	Phe	Cys	Phe	Ala	Thr	Ala	Leu	Xaa	Gly	Arg	Val	Tyr	Tyr	Leu	Xaa	
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His	Pro	Glu	Xaa	Leu	Xaa	Leu	Thr	Xaa	Ala	Arg	Glu	Ala	Cys	Gln	Glu	
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Lys																

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<213> Homo sapiens

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35 40 45

Ile Phe Ser Gln Arg Gly Gly Asn Val Thr Leu Pro Cys Lys Phe Tyr
50 55 60

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65 70 75 80

Lys Trp Thr Lys Leu Thr Ser Asp Tyr Leu Lys Glu Val Asp Val Phe
85 90 95

Val Ala Met Gly His His Arg Lys Ser Tyr Gly Lys Tyr Gln Gly Arg
100 105 110

Val Phe Leu Arg Glu Ser Ser Glu Asn Asp Ala Ser Leu Ile Ile Thr
115 120 125

Asn Ile Met Leu Glu Asp Tyr Gly Arg Tyr Lys Cys Glu Val Ile Glu
130 135 140

Gly Leu Glu Asp Asp Thr Ala Val Val Ala Leu Asn Leu Glu Gly Val
145 150 155 160

Val Phe Pro Tyr Ser Pro Arg Leu Gly Arg Tyr Asn Leu Asn Phe His
165 170 175

Glu Ala Gln Gln Ala Cys Leu Asp Gln Asp Ser Ile Ile Ala Ser Phe
180 185 190

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Asp Gln Leu Tyr Glu Ala Trp Arg Ser Gly Leu Asp Trp Cys Asn Ala	195	200	205
Gly Trp Leu Ser Asp Gly Ser Val Gln Tyr Pro Ile Thr Lys Pro Arg	210	215	220
Glu Pro Cys Gly Gly Lys Asn Thr Val Pro Gly Val Arg Asn Tyr Gly	225	230	235
Phe Trp Asp Lys Glu Arg Ser Arg Tyr Asp Val Phe Cys Phe Thr Ser	245	250	255
Asn Phe Asn Gly Arg Phe Tyr Tyr Leu Ile His Pro Thr Lys Leu Thr	260	265	270
Tyr Asp Glu Ala Val Gln Ala Cys Leu Lys Asp Gly Ala Gln Ile Ala	275	280	285
Lys Val Gly Gln Ile Phe Ala Ala Trp Lys Leu Leu Gly Tyr Asp Arg	290	295	300
Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser Val Arg Tyr Pro Ile Ser	305	310	315
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
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gacgggcaca gctgcacaga gatagacccc tgtgcagacg gccttaacgg aggggtgtcac 180
gagcagcca cctgtaag atg aca ggc ccg ggc aag cac aag tgt gag tgt 231
          Met Thr Gly Pro Gly Lys His Lys Cys Glu Cys
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aaa agt cac tat gtc gga gat ggg ctg aac tgt gag ccg gag cag ctg 279
Lys Ser His Tyr Val Gly Asp Gly Leu Asn Cys Glu Pro Glu Gln Leu
              15              20              25

ccc att gac cgc tgc tta cag gac aat ggg cag tgc cat gca gac gcc 327
Pro Ile Asp Arg Cys Leu Gln Asp Asn Gly Gln Cys His Ala Asp Ala
              30              35              40

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Lys Cys Val Asp Leu His Phe Gln Asp Thr Thr Val Gly Val Phe His
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cta cgc tcc cca ctg ggc cag tat aag ctg acc ttt gac aaa gcc aga	423
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80 85 90	
tcc tat nnc cag aag gcc aag tac cac ctg tgc tca gca ggc tgg ctg	519
Ser Tyr Xaa Gln Lys Ala Lys Tyr His Leu Cys Ser Ala Gly Trp Leu	
95 100 105	
gag acc ggg cgg gtt gcc tac ccc aca gcc ttc gcc tcc cag aac tgt	567
Glu Thr Gly Arg Val Ala Tyr Pro Thr Ala Phe Ala Ser Gln Asn Cys	
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Gly Ser Gly Val Val Gly Ile Val Asp Tyr Gly Pro Arg Pro Asn Lys	
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Ser Glu Met Trp Asp Val Phe Cys Tyr Arg Met Lys Asp Val Asn Cys	
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Thr Xaa Lys Val Gly Tyr Val Gly Asp Gly Phe Ser Tyr Ser Gly Asn	
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Glu Val Leu Ala Tyr Ser Asn Ser Ser Ala Arg Gly Arg Ala Phe Leu	
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gaa cac ctg act gac ctg tcc atc cgc ggc acc ctc ttt gtn cca cag	855
Glu His Leu Thr Asp Leu Ser Ile Arg Gly Thr Leu Phe Val Pro Gln	
205 210 215	

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Leu	Gln	Asp	Asn	Gly	Gln	Cys	His	Ala	Asp	Ala	Lys	Cys	Val	Asp	Leu	
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His	Phe	Gln	Asp	Thr	Thr	Val	Gly	Val	Phe	His	Leu	Arg	Ser	Pro	Leu	
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Glu	Ala	Ala	Thr	Met	Ala	Thr	Tyr	Asn	Gln	Leu	Ser	Tyr	Xaa	Gln	Lys	
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Tyr	Val	Gly	Asp	Gly	Phe	Ser	Tyr	Ser	Gly	Asn	Leu	Leu	Gln	Val	Leu	
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Ser	Asn	Ser	Ser	Ala	Arg	Gly	Arg	Ala	Phe	Leu	Glu	His	Leu	Thr	Asp	
		195				200						205				
Leu	Ser	Ile	Arg	Gly	Thr	Leu	Phe	Val	Pro	Gln	Asn	Ser	Gly	Leu	Gly	
	210					215					220					

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Glu Asn Glu Thr Leu Ser Gly Arg Asp Ile Glu His His Leu Ala Asn
225 230 235 240

Val Ser Met Phe Phe Tyr Asn Asp Leu Val Asn Gly Thr Thr Leu Gln
245 250 255

Thr Arg Leu Gly Ser Lys Leu Leu Ile Thr Asp Arg Gln Asp Pro Leu
260 265 270

His Pro Thr Glu Thr Arg Cys Val Asp Gly Arg Asp Thr Leu Glu Trp
275 280 285

Asp Ile Cys Ala Ser Asn Gly Ile Thr His Val Ile Ser Arg Xaa Leu
290 295 300

Lys Ala Pro Pro Ala Pro Val Thr Leu Xaa His Thr Gly Leu Gly Xaa
305 310 315 320

Gly Ile Phe Xaa Xaa Ile Ile Leu Val Thr Gly Ala Val Ala Leu Ala
325 330 335

Ala Tyr Ser Tyr Phe Arg Ile Asn Arg Lys Thr Ile Gly Phe Xaa His
340 345 350

Phe

<210> 12

<211> 275

<212> PRT

<213> Mus musculus

<400> 12

Met Val Val Leu Leu Cys Leu Cys Val Leu Leu Trp Glu Glu Ala His
1 5 10 15

Gly Trp Gly Phe Lys Asn Gly Ile Phe His Asn Ser Ile Trp Leu Glu
20 25 30

Gln Ala Ala Gly Val Tyr His Arg Glu Ala Arg Ala Gly Arg Tyr Lys
35 40 45

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Leu	Thr	Tyr	Ala	Glu	Ala	Lys	Ala	Val	Cys	Glu	Phe	Glu	Gly	Gly	Arg
50						55					60				
Leu	Ala	Thr	Tyr	Lys	Gln	Leu	Glu	Ala	Ala	Arg	Lys	Ile	Gly	Phe	His
65					70					75					80
Val	Cys	Ala	Ala	Gly	Trp	Met	Ala	Lys	Gly	Arg	Val	Gly	Tyr	Pro	Ile
				85					90					95	
Val	Lys	Pro	Gly	Pro	Asn	Cys	Gly	Phe	Gly	Lys	Thr	Gly	Ile	Ile	Asp
			100					105					110		
Tyr	Gly	Ile	Arg	Leu	Asn	Arg	Ser	Glu	Arg	Trp	Asp	Ala	Tyr	Cys	Tyr
	115						120					125			
Asn	Pro	His	Ala	Lys	Glu	Cys	Gly	Gly	Val	Phe	Thr	Asp	Pro	Lys	Arg
130						135					140				
Ile	Phe	Lys	Ser	Pro	Gly	Phe	Pro	Asn	Glu	Tyr	Asp	Asp	Asn	Gln	Val
145					150					155				160	
Cys	Tyr	Trp	His	Ile	Arg	Leu	Lys	Tyr	Gly	Gln	Arg	Ile	His	Leu	Ser
				165					170					175	
Phe	Leu	Asp	Phe	Asp	Leu	Glu	His	Asp	Pro	Gly	Cys	Leu	Ala	Asp	Tyr
			180					185					190		
Val	Glu	Ile	Tyr	Asp	Ser	Tyr	Asp	Asp	Val	His	Gly	Phe	Val	Gly	Arg
	195						200					205			
Tyr	Cys	Gly	Asp	Glu	Leu	Pro	Glu	Asp	Ile	Ile	Ser	Thr	Gly	Asn	Val
210						215					220				
Met	Thr	Leu	Lys	Phe	Leu	Ser	Asp	Ala	Ser	Val	Thr	Ala	Gly	Gly	Phe
225					230					235					240
Gln	Ile	Lys	Tyr	Val	Thr	Val	Asp	Pro	Ala	Ser	Lys	Ser	Ser	Gln	Ala
				245					250					255	
Lys	Asn	Thr	Ser	Thr	Thr	Gly	Asn	Lys	Lys	Phe	Leu	Pro	Gly	Arg	Phe
			260					265					270		

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Ser His Leu
275

<210> 13
<211> 44
<212> DNA
<213> artificial sequence

<220>
<223> contains an EcoRI restriction site

<400> 13
gcagcaggat ccatgatgga ccagggctgc cgggaaatcc ttac

44

<210> 14
<211> 44
<212> DNA
<213> artificial sequence

<220>
<223> contains a XhoI restriction site

<400> 14
gcagcatcta gatcacttga ctgtgaggat cctctgggtg tcag

44

<210> 15
<211> 45
<212> DNA
<213> artificial sequence

<220>
<223> contains an EcoRI restriction site

<400> 15
gcagcaggat ccatgggtcac ttgtacctgc ctgcccgact acgag

45

<210> 16
<211> 45
<212> DNA
<213> artificial sequence

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<220>
<223> contains a XhoI restriction site

<400> 16
gcagcaggat ccatgggtcac ttgtacctgc ctgcccgact acgag 45

<210> 17
<211> 48
<212> DNA
<213> artificial sequence

<220>
<223> contains an EcoRI restriction site

<400> 17
gcagcaggat ccatgggcct gttgctcctg gtccattgc tctgctg 48

<210> 18
<211> 46
<212> DNA
<213> artificial sequence

<220>
<221> misc_feature
<222> (40)
<223> n equals a, t, g or c

<220>
<223> contains a XhoI restriction site

<400> 18
gcagcatcta gaatttttct tggcaggctt cccttgcttn tgtcag 46

<210> 19
<211> 44
<212> DNA
<213> artificial sequence

<220>
<223> contains an EcoRI restriction site

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<400> 19
gcagcaggat ccatgacagg cccgggcaag cacaagtgtg agtg

44

<210> 20
<211> 49
<212> DNA
<213> artificial sequence

<220>
<221> misc_feature
<222> (21)
<223> n equals a, t, g or c

<220>
<223> contains a XhoI restriction site

<400> 20
gcagcatcta gatcaaaatg ntggaagccg attgttttcc ggtttatcc

49

<210> 21
<211> 50
<212> DNA
<213> artificial sequence

<220>
<223> contains a BglII restriction site

<400> 21
gcagcaagat ctgccatcat gatggaccag ggctgccggg aaatccttac

50

<210> 22
<211> 45
<212> DNA
<213> artificial sequence

<220>
<223> contains a XbaI restriction site

<400> 22
gcagcatcta gatcacttga ctgtgaggat cctctgggtg tcagg

45

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<210> 23
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> contains a BglII restriction site

<400> 23
gcagcaagat ctgccatcat ggtcacttgt acctgcctgc ccgactacga g 51

<210> 24
<211> 45
<212> DNA
<213> artificial sequence

<220>
<223> contains an XbaI restriction site

<400> 24
gcagcatcta gatcacttga ctgtgaggat cctctgggtg tcagg 45

<210> 25
<211> 54
<212> DNA
<213> artificial sequence

<220>
<223> contains a BglII restriction site

<400> 25
gcagcaagat ctgccatcat gggcctgttg ctctgggtcc cattgtcct gctg 54

<210> 26
<211> 46
<212> DNA
<213> artificial sequence

<220>
<221> misc_feature
<222> (40)
<223> n equals a, t, g or c

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<220>
<223> contains an XbaI restriction site

<400> 26
gcagcatcta gaatttttct tggcaggctt cccttgcttn tgtcag 46

<210> 27
<211> 50
<212> DNA
<213> artificial sequence

<220>
<223> contains a BglII restriction site

<400> 27
gcagcaagat ctgccatcat gacaggcccg ggcaagcaca agtgtgagtg 50

<210> 28
<211> 49
<212> DNA
<213> artificial sequence

<220>
<221> misc_feature
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<223> n equals a,t,g, or c

<220>
<223> contains a XbaI restriction site

<400> 28
gcagcatcta gatcaaaatg ntggaagccg attgttttcc ggtttatcc 49

<210> 29
<211> 50
<212> DNA
<213> artificial sequence

<220>
<223> contains a BamHI restriction site

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<400> 29
gcagcaagat ctgccatcat gatggaccag ggctgccggg aaatccttac 50

<210> 30
<211> 44
<212> DNA
<213> artificial sequence

<220>
<223> contains an XbaI restriction site

<400> 30
gcagcatcta gatcacttga ctgtgaggat cctctgggtg tcag 44

<210> 31
<211> 54
<212> DNA
<213> artificial sequence

<220>
<223> contains a BamHI restriction site

<400> 31
gcagcaagat ctgccatcat gatggtcact tgtacctgcc tgcccgacta cgag 54

<210> 32
<211> 45
<212> DNA
<213> artificial sequence

<220>
<223> contains an XbaI restriction site

<400> 32
gcagcatcta gatcacttga ctgtgaggat cctctgggtg tcagg 45

<210> 33
<211> 54
<212> DNA
<213> artificial sequence

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<220>
<223> contains a BamHI restriction site

<400> 33
gcagcaagat ctgccatcat gggcctgttg ctcttggtcc cattgctcct gctg 54

<210> 34
<211> 46
<212> DNA
<213> artificial sequence

<220>
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<223> n equals a, t, g or c

<220>
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<400> 34
gcagcatcta gaatttttct tggcaggctt cccttgcttn tgtcag 46

<210> 35
<211> 50
<212> DNA
<213> artificial sequence

<220>
<223> contains a BamHI restriction site

<400> 35
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<210> 36
<211> 49
<212> DNA
<213> artificial sequence

<220>
<221> misc_feature
<222> (21)
<223> n equals a, t, g or c

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<220>
<223> contains an XbaI restriction site

<400> 36
gcagcatcta gatcaaaatg ntggaagccg attgttttcc ggtttatcc 49

<210> 37
<211> 733
<212> DNA
<213> Homo sapiens

<400> 37
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aattcgaggg tgcaccgtca gtcttcctct tcccccaaa acccaaggac accctcatga 120
tctcccgga tcttgaggtc acatgcgtgg tggaggacgt aagccacgaa gaccctgagg 180
tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240
aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300
ggctgaatgg caaggagtac aagtgcgaagg tctccaacaa agccctccca acccccatcg 360
agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420
catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctgggc aaaggcttct 480
atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga 540
ccacgcctcc cgtgctggac tccgacggct cttcttctct ctacagcaag ctcaccgtgg 600
acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggtctgc 660
acaaccacta cagcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc 720
gactctagag gat 733

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